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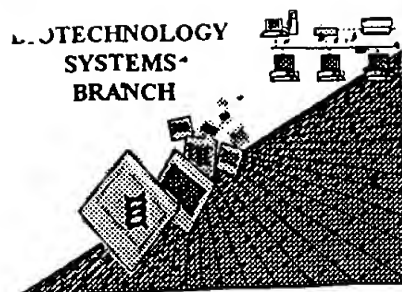
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RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/777430
Source: OIPE
Date Processed by STIC: 10/09/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/777430
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length.	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING

DATE: 10/09/2001

PATENT APPLICATION: US/09/777,430

TIME: 08:29:58

Input Set : A:\4912SEQS.txt

Output Set: N:\CRF3\10092001\I777430.raw

3 <110> APPLICANT: Lyamichev, Victor
 5 <120> TITLE OF INVENTION: CHARGE TAGS AND SEPARATION OF NUCLEIC ACID MOLECULES
 7 <130> FILE REFERENCE: FORS 4912

C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/777,430

C--> 9 <141> CURRENT FILING DATE: 2001-02-06

9 <160> NUMBER OF SEQ ID NOS: 85

11 <170> SOFTWARE: PatentIn version 3.0

13 <210> SEQ ID NO: 1

14 <211> LENGTH: 23

15 <212> TYPE: DNA

16 <213> ORGANISM: synthetic

18 <220> FEATURE:

19 <221> NAME/KEY: misc_feature

20 <222> LOCATION: (1)..(2)

21 <223> OTHER INFORMATION: misc. feature

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38 <211> LENGTH: 30

39 <212> TYPE: DNA

40 <213> ORGANISM: synthetic

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46 <210> SEQ ID NO: 4

47 <211> LENGTH: 30

48 <212> TYPE: DNA

49 <213> ORGANISM: synthetic

51 <400> SEQUENCE: 4

52 cagggggaag ggaagaagaa agcgaaaggt

55 <210> SEQ ID NO: 5

56 <211> LENGTH: 28

57 <212> TYPE: DNA

58 <213> ORGANISM: synthetic

60 <400> SEQUENCE: 5

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65 <211> LENGTH: 30

66 <212> TYPE: DNA

67 <213> ORGANISM: synthetic

69 <400> SEQUENCE: 6

70 tcgacgtcga ctaacccttg gcggaaagcc

Does Not Comply
 Corrected Diskette Needed

Errored:

Synthetic is appropriate
 for an explanation of "Artificial Sequence"
 in the 223 field. — However, "Synthetic"

is not an appropriate response for the
 213 field.

FYI: "Artificial Sequence", "Unknown" and
 species names are the only
 appropriate 213 responses

See Error Summary Sheet item 10.

30

30

28

30

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/777,430

DATE: 10/09/2001

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Input Set : A:\4912SEQS.txt

Output Set: N:\CRF3\10092001\I777430.raw

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 74 <211> LENGTH: 23
 75 <212> TYPE: DNA
 76 <213> ORGANISM: synthetic
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23

82 <210> SEQ ID NO: 8

83 <211> LENGTH: 0

84 <212> TYPE: PRT

85 <213> ORGANISM: Thermus thermophilus

87 <400> SEQUENCE: 8

Does Not Comply
 Corrected Diskette Needed

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93 <213> ORGANISM: Thermus thermophilus

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/777,430

DATE: 10/09/2001

TIME: 08:29:58

Input Set : A:\4912SEQS.txt

Output Set: N:\CRF3\10092001\I777430.raw

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382 gccgcgatgc tcttcagggt ccacaacgag ctctctctgg agggccccc aagcggggcc 2400
384 gaggagggtg cggctttggc caaggaggcc atggagaagg cctatccct cgcctgccc 2460
386 ctggagggtg aggtggggat gggggaggac tggcttccg ccaagggtca ccaccaccac 2520
388 caccac 2526

```

391 <210> SEQ ID NO: 15

392 <211> LENGTH: 0

393 <212> TYPE: PRT

394 <213> ORGANISM: Thermus thermophilus

396 <400> SEQUENCE: 15

W--> 397 000

399 <210> SEQ ID NO: 16

400 <211> LENGTH: 31

401 <212> TYPE: DNA

402 <213> ORGANISM: synthetic

404 <400> SEQUENCE: 16

405 gcctgcaggg gcggccgcgt gcaccggggc a

31

408 <210> SEQ ID NO: 17

409 <211> LENGTH: 26

410 <212> TYPE: DNA

411 <213> ORGANISM: synthetic

413 <400> SEQUENCE: 17

414 ctcttggaac cttcgaacac caccac

26

417 <210> SEQ ID NO: 18

418 <211> LENGTH: 23

419 <212> TYPE: DNA

420 <213> ORGANISM: synthetic

422 <400> SEQUENCE: 18

423 gtcttgccc atatggaggc cac

23

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/777,430

DATE: 10/09/2001

TIME: 08:29:59

Input Set : A:\4912SEQS.txt

Output Set: N:\CRF3\10092001\I777430.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:25 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:88 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:196 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:397 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:525 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:635 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (23) SEQUENCE:
L:745 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (26) SEQUENCE:
L:753 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (27) SEQUENCE:
L:761 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (28) SEQUENCE:
L:769 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (29) SEQUENCE:
L:777 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (30) SEQUENCE:
L:797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:872 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1024 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:
L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1086 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:1116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:1256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77
L:1457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82